

ESTIMATION OF GENETIC VARIABILITY IN PEA (*PISUM SATIVUM* L.)

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Genetic variability estimation was conducted in twelve genotypes of peas during growing season 2011-12. Analysis of variance was highly significant for all characters studied except plant height present high scope for selection. The highest genotypic and phenotypic co-efficient of variation were recorded for pod per plant (31.62, 31.99) followed by seed yield per plant (22.87, 23.65), cluster per plant (18.81, 20.21) and lowest was noted for days to maturity (1.88, 2.15). High heritability with high genetic advance as percent of means was recorded for pod per plant (0.98, 64.37%) followed by seed yield (0.94, 45.56%). The lowest was observed for plant height (0.35, 13.80%). The study indicates that emphasis should be given to these characters for yield improvement.

Keywords: Genetic Variability, heritability, genetic advances, Peas

INTRODUCTION

Vegetable are rich in nutrition and are very dense source of bioactive component (Shakeel *et al.*, 2013). Pea (*Pisumsativum* L.) is a prominent vegetable crop of winter season in Pakistan. Its area was 15.8 thousand hectares with production of 105.0 thousand tones during 2012. Its family is Leguminaceae and native to central or Southeast Asia (Warren *et al.*, 1956). Pea has great nutrient value and contains vitamin A, B and C, along with minerals, dietary fiber and antioxidant compounds (Urbano *et al.*, 2003). A great diversity is present for pea breeder that may be used to evolve high yielding varieties. Javaid *et al.* (2002) evaluated the local and exotic pea germplasm for earliness and grain yield through simple selection and suggested that elite genotypes can be used in hybridization program for pea improvement. Ashraf *et al.* (1981) studied the positive and significant correlation between first picking, pod and seed weight per plant in eight pea's cultivars. Qamar *et al.* (1993) referred that plant height, number leaves and branches were the most important characters and selection may be done on the basis of these characters in forage pea. Success of hybridization program is dependent on genetic variation in breeding material. Investigation was done to estimate genetic variability for the selection of desirable genotypes for various quantitative traits.

MATERIALS AND METHODS

The experiment was conducted at Pulses Research Institute, Faisalabad during summer 2012. Experimental site lies between 30.35-41.47°N latitude and 72.08-73.40°E longitude at an elevation of 184.4 m above sea level (Rana *et al.*, 2014). The experiment was conducted in Randomized Complete Block Design with three replications. Sowing was

done in first week of July. Plant to plant and row to row distance were maintained 15 cm and 30 cm, respectively. Twelve genotypes were evaluated for variation. These genotypes were:

1. DP-01-12	7. DP-07-12
2. DP-02-12	8. DP-08-12
3. DP-03-12	9. DP-09-12
4. DP-04-12	10. Climax
5. DP-05-12	11. DP-11-01
6. DP-06-12	12. NO-267

Table 1: Grand mean, mean sum of square and co-efficient of variance in peas

Characters	Grand Means	MS	CV
Cluster per plant	16.142	19.8597**	7.39
Pod per plant	31.736	203.773**	4.88
Plant height(cm)	64.023	199.809NS	15.27
Pod length (cm)	5.7238	2.369*	13.30
Daysto50% flowering	89.375	412.466**	1.35
Days to maturity	127.63	13.2841**	1.03
Seed per pod	5.3183	0.67019**	5.86
Seed Yield	439.29	20885.6**	6.02

**=Significant at 1% level of significance, *=Significant at 5% level of significance, NS=Non-significant.

Data were collected on number of cluster per plant, pods per plant, plant height, pod length, days to 50% flowering and maturity, seed per pod and seed yield per plant. The data were statistically analyzed, means were compared using Tukey test at 0.05 level of probability (Steel and Torrie, 1984). Estimation of heritability and expected genetic advance of variance components were estimated according to the formula given by Singh and Choudhary (1979). Heritability (h) genotypic variance/phenotypic variance.

Table 2: Mean values of 12 genotypes for cluster per plant, pod per plant, plant height (cm), Length per pod (cm), days to 50% flowering, days to maturity, Seed per pod and seed yield per plot (g).

Genotypes	Cluster per plant	Pod per plant	Plant height (cm)	Length per pod (cm)	Days to 50% flowering	Days to maturity	Seed per pod	Seed yield per plot (g)
Dp-01-12	16.17 b-e	38.00 a	68.33	6.23ab	96.5 b	130.0 ab	4.67 b	297.0 e
Dp-02-12	12.67 de	28.66 c	76.17	4.81 b	89.5 c	125.5 bc	5.83ab	410.0 cd
Dp-03-12	15.33 cde	36.33 ab	81.67	4.37 b	100.5 ab	129.5 abc	5.63ab	456.0 bc
Dp-04-12	13.00 de	27.33 c	65.50	6.68ab	101.5 a	133.5 a	4.83 b	391.5 cde
Dp-05-12	16.83 bcd	30.33 bc	69.63	5.27 b	97.5 ab	129.0 abc	5.16 b	403.0 cde
DP-06-12	11.50 e	41.00 a	55.33	5.35 b	96.5 b	125.5 bc	4.83 b	544.0 ab
DP-07-12	15.67 b-e	36.50 ab	54.33	5.77ab	96.5 b	127.0 bc	4.66 b	572.0 a
DP-8-12	20.17 ab	39.66 a	63.67	5.80ab	97.5 ab	125.5 bc	5.50ab	465.0 bc
DP-09-12	15.02 cde	36.33 ab	70.33	6.07ab	98.0 ab	128.5 abc	5.63ab	348.5 de
Climax	19.50 abc	41.35 a	60.50	8.45 a	63.5 e	124.5 c	5.20 b	322.0 de
Dp-11-01	22.10 a	15.69 d	46.50	5.16 b	65.0 e	126.0 bc	6.67 a	635.5 a
N0-267	15.78 b-e	9.67 d	56.33	4.75 b	70.0 d	127.0 bc	5.23 b	427.0 cd
Tukey HSD Value	4.82	6.25	NS	3.07	4.88	5.32	1.26	106.77

NS=Non-significant

Table 3: Genetic parameter for various quantitative traits of pea genotypes

Characters	Genotypic coefficient of variance	Phenotypic coefficient of variance	Environmental variance	Environmental coefficient of variance	Heritability	Genetic advance	Genetic advance (%)
Cluster per plant	18.81	20.21	19.86	27.61	0.87	5.82	36.06
Pod per plant	31.62	31.99	203.77	44.98	0.98	20.43	64.37
Plant height (cm)	11.28	18.98	199.81	22.08	0.35	8.84	13.80
Length per pod (cm)	16.53	21.21	2.37	26.89	0.61	1.52	26.53
Days to 50% flowering	16.04	16.10	412.466	22.72	0.99	29.43	32.92
Days to maturity	1.88	2.15	13.2841	2.86	0.77	4.34	3.40
Seed per pod	10.07	11.65	0.67019	15.39	0.75	0.95	17.92
Seed yield per plot (g)	22.87	23.65	20885.6	32.90	0.94	200.14	45.56

$$\text{Heritability (h)} = \frac{\sigma^2_g}{\sigma^2_p}$$

Where σ^2_g and σ^2_p are genotypic and phenotypic

variances, respectively.

$$\text{Genetic advance} = Kh^2\sigma_p$$

Where

K = selection differential at 5% selection intensity = 2.06

h^2 = heritability coefficient

σ_p = phenotypic standard deviation

RESULTS AND DISCUSSION

The analysis of variance for different traits showed that mean sum of squares due to genotypes exhibit significant differences for most of the traits under observation at 1% probability level except for pod length which was significant at 5% probability level and plant height was non-significant at both levels of significance (Table 1). It shows large amount of genetic variability among pea genotypes. Data regarding the comparison of means (Table 2) show that cluster per plant indicated that maximum cluster was attained by genotype DP-8-12(22.10), while minimum in genotype DP-06-12 (11.50). All other genotypes were intermediate between these two genotypes. Maximum numbers of pods per plant were noted for the genotype Climax (41.35) and minimum for genotype N0-267(9.67). The remaining values were between these ranges. Plant

height relevant data indicated that statistically there were no significant differences among the means of tested genotypes. Pod length means comparison was statistically significant and maximum pod length was recorded in genotype Climax (8.45 cm) while minimum was recorded in DP-03-12 (4.37 cm). Days to 50% flowering and days to maturity also show significant difference among the means of observed genotypes. Data regarding seed per pod showed significant differences among genotypes. Maximum seed per pod were produced by genotype DP-11-01 (6.67) and minimum were produced by genotype DP-07-12 (4.66). Genotype DP-11-01 produced maximum yield per plot (635.5 g) and minimum was produced by genotype DP-01-12(297 g). Similar findings for the genetic variability among different quantitative traits in field pea were reported by Kumar *et al.* (2003); Jitendra *et al.* (2010) and Kumar *et al.* (2013).

These genotypic and phenotypic variations, heritability and genetic advance expressed as percent of mean have been presented in Table 3. The highest estimates of genotypic and phenotypic variations were noted for number of pods per plant (31.62, 31.99), seed yield per plot (22.87, 23.65) and cluster per plant (18.81, 20.21), exhibit variation and effect of environment on the expression of the characters. The lowest estimates were noted for days to maturity (1.8, 2.15), seed per pod (10.07, 11.65), plant height (11.28, 18.98), days to 50% flowering (16.04, 16.10) indicate the little role of environment on the expression of these traits. These studies confirm the findings of Kumar *et al.* (2013).

Heritability estimated range is from 0.99 to 0.35. Highest heritability (0.99) was noted for days to 50% flowering followed by pods per plant (0.98), seed yield per plot (0.94) and cluster per plant (0.87). These results are in line with the findings of Pallavi and Pandey (2013). Only heritability is not sufficient to select the best genotype but with genetic advance it is more reliable (Johnson *et al.*, 1955). High heritability with high genetic advance for number of pods per plant (0.98, 64.37%) followed by seed yield per plot (0.94, 45.56), cluster per plant (0.87, 36.06) and days to 50% flowering (0.99, 32.92%). Similar results were reported by Raffi and Nath (2004) in pea. High heritability associated with high genetic advance indicates additive gene effects and selection may be effective on basis of these traits. Pure line selection, mass selection and pedigree selection may be effective in case of self-pollinated crop such as peas. Low heritability with low genetic advance was noted for plant height (0.35, 13.80) showed that there is high environment influence on the character and influence would be ineffective. It is clear that genotypes of peas having more number of pods per plant and the number of clusters per plant should be selected for the improvement in the seed yield of pea.

CONCLUSION

High genotypic and phenotypic co-efficient of variation were recorded. Likewise, high heritability with high genetic advance as percent of means was recorded for pod per plant during the experiment. So the results show that genotypes of peas having more number of pods per plant should be selected for the improvement in the seed yield of pea.

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